



# UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE  
United States Patent and Trademark Office  
Address: COMMISSIONER FOR PATENTS  
P.O. Box 1450  
Alexandria, Virginia 22313-1450  
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
-----------------	-------------	----------------------	---------------------	------------------

10/715,066

11/17/2003

Timothy O'Brien

022438.45514

6392

7590  
McTavish Patent Firm  
429 Birchwood Courts  
Birchwood, MN 55110

01/18/2007

EXAMINER

REDDIG, PETER J

ART UNIT

PAPER NUMBER

1642

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
--	-----------	---------------

3 MONTHS

01/18/2007

PAPER

**Please find below and/or attached an Office communication concerning this application or proceeding.**

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

**Office Action Summary**

Application No.

10/715,066

Applicant(s)

O'BRIEN ET AL.

Examiner

Peter J. Reddig

Art Unit

1642

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --  
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 17 November 2006.  
2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.  
3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 1, 2 and 21 is/are pending in the application.  
4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.  
5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.  
6) ☒ Claim(s) 1, 2, and 21 is/are rejected.  
7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.  
8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☐ The specification is objected to by the Examiner.  
10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).  
11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).  
a) ☐ All b) ☐ Some \* c) ☐ None of:  
1. ☐ Certified copies of the priority documents have been received.  
2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.  
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- 1) ☒ Notice of References Cited (PTO-892)  
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)  
3) ☐ Information Disclosure Statement(s) (PTO/SB/08)  
Paper No(s)/Mail Date \_\_\_\_\_.  
4) ☐ Interview Summary (PTO-413)  
Paper No(s)/Mail Date. \_\_\_\_\_.  
5) ☐ Notice of Informal Patent Application  
6) ☒ Other: Appendix 1.

### **DETAILED ACTION**

1. The Amendment filed November 17, 2006 in response to the Office Action of August 7, 2006 is acknowledged and has been entered. Previously pending claims 3-20 have been cancelled, claim 1 has been amended, and new claim 21 has been added.
2. Claims 1, 2, and 21 are currently being examined.
3. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

### ***Response to Amendment***

4. The declaration under 37 CFR 1.132 filed November 17, 2006 is sufficient to overcome the rejection of claims 1 and 2 based upon O'Brien et al. (Tumor Biology, 2002 May-Jun; 23:154-69, IDS).
5. The following rejections are being maintained:

### ***Double Patenting***

6. Claim 2 remains provisionally rejected under 35 USC 101 as claiming the same invention as that of claim 25 of co-pending application 10/475,117.

### ***New Grounds of Rejection***

### ***Claim Rejections - 35 USC § 112***

7. Claims 1 and 21 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Art Unit: 1642

The limitation of a polypeptide comprising residues 1-10,427 of SEQ ID NO: 5 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 has no clear support in the specification and the claims as originally filed. Examiner's review of the specification did not reveal support for the newly added limitation. Applicants pointed to support for amended claim 1 in originally filed claims 1, 4, 14, and 15, SEQ ID NO: 1, 4, and 5 and paragraphs 0009, 0011, and 0041. A review of originally filed claims 1, 4, 14, and 15 revealed support for 1) an isolated nucleic acid molecule encoding CA125, 4) the isolated nucleic acid molecule of claim 2 wherein said molecule is a fragment thereof, 14) a polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequence set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to said sequence; (c) a conservative variant of an one of (a) to (b); and (d) a fragment of any one of (a) to (c), and 15) a purified antibody that selectively binds to an amino acid sequence of the CA125 protein: (a) wherein the amino acid sequence of the CA125 protein comprises the amino acid sequence set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to said sequence; (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c). A review of the cited portions of the specification revealed support for SEQ ID NOs: 1-5, the genomic sequence of CA125, a full-length cDNA for CA125, and a CA125 protein, and the domain structure of the CA125 gene and protein. The suggested support is not found persuasive because there is nothing in the specification to suggest the limitation of a polypeptide comprising residues 1-10,427 of SEQ ID NO: 5 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5. Applicant is invited to submit evidence pointing to page

Art Unit: 1642

and line number in the specification wherein support for the newly added limitation can be found.

8. If applicant were able to overcome the rejections set forth above, claims 1 and 21 would still be rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid molecule encoding CA125 (SEQ ID NO: 5) or a fragment thereof, an isolated nucleic acid molecule that encodes a polypeptide **consisting of** residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5, and an isolated nucleic acid molecule encoding CA125, wherein the isolated nucleic acid molecule **consists of** SEQ ID NO: 1 or a fragment thereof, does not reasonably provide enablement for an isolated nucleic acid molecule encoding **a fragment of SEQ ID NO: 5**, wherein the isolated nucleic acid molecule encodes a polypeptide **comprising** residues 1-10,427 **or a fragment of residues 1-10,427** of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 or wherein the isolated nucleic acid molecule **comprises** SEQ ID NO: 1 or a fragment thereof. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The claims are drawn to an isolated nucleic acid molecule encoding a polypeptide comprising a fragment of CA125 (SEQ ID NO: 5), wherein the isolated nucleic acid molecule encodes a polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 and wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof.

Art Unit: 1642

and line number in the specification wherein support for the newly added limitation can be found.

8. If applicant were able to overcome the rejections set forth above, claims 1 and 21 would still be rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid molecule encoding CA125 (SEQ ID NO: 5) or a fragment thereof, an isolated nucleic acid molecule that encodes a polypeptide **consisting of** residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5, and the isolated nucleic acid molecule encoding CA125, wherein the isolated nucleic acid molecule **consists of** SEQ ID NO: 1 or a fragment thereof, does not reasonably provide enablement for an isolated nucleic acid molecule encoding **a fragment of SEQ ID NO: 5**, wherein the isolated nucleic acid molecule encodes a polypeptide **comprising** residues 1-10,427 **or a fragment of residues 1-10,427** of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 or wherein the isolated nucleic acid molecule **comprises** SEQ ID NO: 1 or a fragment thereof. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The claims are drawn to an isolated nucleic acid molecule encoding a polypeptide comprising a fragment of CA125 (SEQ ID NO: 5), wherein the isolated nucleic acid molecule encodes a polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 and wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof.

This means that an antibody that selectively binds SEQ ID NO: 5 can also recognize **any** polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or **any** polypeptide encoded by an isolated nucleic acid molecule comprising SEQ ID NO: 1 or a fragment thereof.

The specification teaches that CA125 is an antigenic determinant located on the surface of ovarian carcinoma cells with essentially no expression in normal adult ovarian tissue. The specification teaches that elevated in the sera of patients with ovarian adenocarcinoma, CA125 has played a critical role for more than 15 years in the management of these patients relative to their response to therapy and also as an indicator of recurrent disease, see para. [0003].

The specification teaches that SEQ ID NO: 1 is a DNA sequence showing the 5' upstream region and the amino terminal portion of the CA125 molecule, see 2<sup>nd</sup> sentence of para. [0009].

The specification teaches that SEQ ID NO: 5 is a CA125 protein and SEQ ID NO: 4 is a full-length cDNA for CA125, see last two lines of para. [0009].

One cannot extrapolate the teachings of the specification to the scope of the claims because polypeptides comprising residues 1-10,427 of SEQ ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof contain undefined sequences in addition to those in SEQ ID NO: 5 and one of skill in the art could not predict that an antibody that recognizes and binds CA125 as shown in SEQ ID NO: 5 will recognize and bind the broadly claimed CA125 protein polypeptides comprising fragments of said protein because protein biochemistry is unpredictable and the undefined additional amino acids in a polypeptide comprising residues 1-10,427 of SEQ

Art Unit: 1642

ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof encompassed by the claims would be expected to alter the conformation of the protein and if the antibody binding determinants are not shared by the altered CA125 antigen, the antibodies will not bind.

In particular, protein chemistry is probably one of the most unpredictable areas of biotechnology. For example, Bowie et al (Science, 1990, 257:1306-1310) teach that an amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of these proteins to fold into unique three-dimensional structures that allows them to function and carry out the instructions of the genome (col 1, p. 1306). Bowie et al further teach that while it is known that many amino acid alterations are possible in any given protein, the position within the protein's sequence where such amino acid alterations can be made with a reasonable expectation of maintaining function are limited. Certain positions in the sequence are critical to the three dimensional structure/function relationship and these regions can tolerate only conservative alterations or no alterations. However, the specification provides no guidance as to which of the broadly claimed encoded polypeptides comprising CA125 fragments comprise structures or residues that are critical to the binding of antibodies to CA125. The artisan is left to random experimentation in order to determine which of the broadly claimed CA125 proteins will be bound by an antibody that selectively binds to SEQ ID NO: 5. Random experimentation is undue.

Furthermore, the exquisite sensitivity of antibody binding to alterations of even a single amino acid is well known in the art. For example, Coleman et al. (Research in



Art Unit: 1642

Immunology, 1994; 145(1): 33-36) teach single amino acid changes in an antigen can effectively abolish antibody antigen binding. Furthermore, Abaza et al. (Journal of Protein Chemistry, Vol. 11, No. 5, 1992, pages 433-444, see abstract in particular) teach single amino acid substitutions outside the antigenic site on a protein affects antibody binding. These references demonstrate that even a single amino acid alteration or what appears to be an inconsequential chemical modification will often dramatically affect the biological activity and characteristics of a binding protein.

Given the above, and given that the residues of SEQ ID NO: 5 that are critical to binding and recognition by an antibody that selectively binds to SEQ ID NO: 5, or any other antibody, have not been identified, it could not be predicted which protein comprising residues 1-10,427 of SEQ ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof would be bound by an antibody that selectively binds to SEQ ID NO: 5 and one would not know how to make the claimed invention. Although Applicants might argue that one of ordinary skill could screen for the species that would function as claimed, in particular, screening assays do not enable the claimed invention because the court found in (*Rochester v. Searle*, 358 F.3d 916, Fed Cir., 2004) that screening assays are not sufficient to enable an invention because they are merely a wish or plan for obtaining the claimed chemical invention. Given the exquisite sensitivity of antibodies to changes in the amino acid sequence of the target antigen, it would not be expected and could not be predicted that the invention would function as claimed in the absence of further guidance. Given the teaching of Bowie et al that the amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of these proteins to fold into unique three-

Art Unit: 1642

dimensional structures that allows them to function and carry out the instructions of the genome, it is clear that the folding and shape of the undefined polypeptides comprising residues 1-10,427 of SEQ ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof cannot be predicted. The specification provides neither information nor guidance on how to predictably identify which of the broadly claimed polypeptides comprising residues 1-10,427 of SEQ ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof will be bound by an antibody that selectively binds to SEQ ID: 5.

The specification provides insufficient guidance with regard to these issues and provides no working examples which would provide guidance to one skilled in the art and no evidence has been provided which would allow one of skill in the art to predict that the invention would function as broadly claimed with a reasonable expectation of success. For the above reasons, it appears that undue experimentation would be required to practice the claimed invention.

9. Claims 1 and 21 are rejected under 35 USC 112, first paragraph, as lacking an adequate written description in the specification.

The claims are drawn to an isolated nucleic acid molecule encoding CA125 (SEQ ID NO: 5) or a fragment thereof, wherein the isolated nucleic acid molecule encodes a polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 and wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof.

Art Unit: 1642

Although drawn to DNA arts, the findings in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) and Enzo Biochem, Inc. V. Gen-Probe Inc. are relevant to the instant claims. The Federal Circuit addressed the application of the written description requirement to DNA-related inventions in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997). The court stated that "[a] written description of an invention involving a chemical genus, like a description of a chemical species, requires a precise definition, such as by structure, formula, [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." *Id.* At 1567, 43 USPQ2d at 1405. The court also stated that

a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA" without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is.

*Id.* At 1568, 43 USPQ2d at 1406. The court concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." *Id.*

Finally, the court addressed the manner by which a genus of cDNAs might be described. "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." *Id.*

The Federal Circuit has recently clarified that a DNA molecule can be adequately described without disclosing its complete structure. See Enzo Biochem, Inc. V. Gen-Probe Inc., 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002). The Enzo court adopted the standard that "the written description requirement can be met by 'show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics.... i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics. " Id. At 1324, 63 USPQ2d at 1613 (emphasis omitted, bracketed material in original).

The inventions at issue in Lilly and Enzo were DNA constructs per se, the holdings of those cases are also applicable to claims such as those at issue here.

Thus, the instant specification may provide an adequate written description of an isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 per Lilly by structurally describing a representative number of isolated nucleic acid molecules encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 or by describing "structural features common to the members of the genus, which features constitute a substantial portion of the genus." Alternatively, per Enzo, the specification can show that the claimed invention is complete "by disclosure of sufficiently detailed, relevant identifying

Art Unit: 1642

characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics."

In this case, the specification does not describe an isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 in a manner that satisfies either the Lilly or Enzo standards. The specification does not provide the complete structure of any isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5, nor does the specification provide any partial structure of such isolated nucleic acid, nor any physical or chemical characteristics of the isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 nor any functional characteristics coupled with a known or disclosed correlation between structure and function other than SEQ ID NOS: 1 and 4. Although the specification discloses SEQ ID NOS: 1 and 4, this does not provide a description of an isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 the standard set out in Enzo.

The specification also fails to describe the isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 by the test set out in Lilly. The specification describes only SEQ ID NOs: 1 and 4. Therefore, it necessarily fails to describe a "representative number" of such species. In addition, the specification also does not describe "structural features common to the members of the genus, which features constitute a substantial portion of the genus.

Thus, the specification does not provide an adequate written description of the isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 that is required to practice the claimed invention.

Some of the arguments drawn to the previous rejection of claims 3 and 4 are relevant to the instant rejection. In regards to claim 1 and the written description requirement Applicants argue that the complete structure of "An isolated nucleic acid molecule encoding CA 125 (SEQ ID NO: 5) or a fragment thereof" is disclosed in the specification and recited in claim 1.

Applicants argue that the complete structures of genomic nucleic acid sequences encoding SEQ ID NO: 5 and fragments thereof are disclosed in the specification in SEQ ID NOS: 1-3.

Applicants argue that the complete structure of a cDNA encoding SEQ ID NO: 5 is disclosed as SEQ ID NO: 4. Applicants argue that the complete structure of any other nucleic acid encoding SEQ ID NO: 5 or a fragment thereof is disclosed by the disclosure of SEQ ID NO: 5 in the

Art Unit: 1642

specification and by the knowledge of the genetic code. Applicants argue that the complete and exact structure of every possible species within the genus claimed by claim 1 is disclosed in the specification.

In regards to University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) Applicants argue that the claims 1 and 2 recite the precise structure of CA125 (SEQ ID NO: 5). Applicant argues that this also, with knowledge of the genetic code, inherently discloses the structure of every nucleic acid encoding SEQ ID NO: 5 or a fragment thereof.

Applicants' arguments have been carefully considered, but have not been found persuasive because applicant is arguing limitations not recited in the claims as currently constituted. The comprising language of claim 1 does not limit claim to sequences contained only in SEQ ID NO: 4 or 5, rather claim 1 encompasses any isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof encoding a polypeptide recognized by an antibody that selectively binds to SEQ ID NO: 5. Thus, numerous unknown and undefined amino acid additions to a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 and polypeptides encoded by nucleic acids comprising SEQ ID NO: 1 or fragments thereof are encompassed by the claims and for the reasons set forth above, neither the specification nor the claims as originally filed meet the written description requirements of 35 USC 112, first paragraph.

***Claim Rejections - 35 USC § 102***

Art Unit: 1642

10. Claim 1 and 21 are rejected under 35 U.S.C. 102(b) as being anticipated by DOE Joint Genome Institute, Homo sapiens chromosome 19 clone CTD-2596O15, LOW-PASS SEQUENCE SAMPLING, Accession No. AC016584, Version AC016584.2, GI 6758722, January 26, 2000 as evidenced by Appendix 1.

The DOE Joint Genome Institute teaches nucleotide sequences that are homologous to CA125 nucleic acids that encode fragments of residues 1-10,427 of SEQ ID NO: 5.

Although the reference does not specifically state that the nucleic acid sequences are a CA125 sequence and that an antibody that selectively binds to SEQ ID NO: 5 will recognize the protein encoded by the nucleic acid of Accession No. AC016584, Version AC016584.2, the claimed product appears to be the same as the prior art product, absent a showing of unobvious differences. The office does not have the facilities and resources to provide the factual evidence needed in order to establish that the product of the prior art does not possess the same material, structural and functional characteristics of the claimed product. In the absence of evidence to the contrary, the burden is on the applicant to prove that the claimed product is different from that taught by the prior art and to establish patentable differences. See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977).

11. All other objections and rejections recited in the Office Action of August 7, 2006 are withdrawn.

12. No claims allowed.

13. This action is a **final rejection** and is intended to close the prosecution of this application. Applicant's reply under 37 CFR 1.113 to this action is limited either to an appeal to



the Board of Patent Appeals and Interferences or to an amendment complying with the requirements set forth below.

If applicant should desire to appeal any rejection made by the examiner, a Notice of Appeal must be filed within the period for reply identifying the rejected claim or claims appealed. The Notice of Appeal must be accompanied by the required appeal fee.

If applicant should desire to file an amendment, entry of a proposed amendment after final rejection cannot be made as a matter of right unless it merely cancels claims or complies with a formal requirement made earlier. Amendments touching the merits of the application which otherwise might not be proper may be admitted upon a showing a good and sufficient reasons why they are necessary and why they were not presented earlier.

A reply under 37 CFR 1.113 to a final rejection must include the appeal from, or cancellation of, each rejected claim. The filing of an amendment after final rejection, whether or not it is entered, does not stop the running of the statutory period for reply to the final rejection unless the examiner holds the claims to be in condition for allowance. Accordingly, if a Notice of Appeal has not been filed properly within the period for reply, or any extension of this period obtained under either 37 CFR 1.136(a) or (b), the application will become abandoned.

14. Applicants' amendment necessitated the new grounds of rejection. Thus, **THIS ACTION IS MADE FINAL**. Applicant is reminded of the extension of time policy as set forth in 37 C.F.R. ' 1.136(a).

A SHORTENED STATUTORY PERIOD FOR RESPONSE TO THIS FINAL ACTION IS SET TO EXPIRE THREE MONTHS FROM THE DATE OF THIS ACTION. IN THE EVENT A FIRST RESPONSE IS FILED WITHIN TWO MONTHS OF THE MAILING DATE

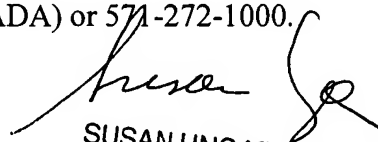
Art Unit: 1642

OF THIS FINAL ACTION AND THE ADVISORY ACTION IS NOT MAILED UNTIL AFTER THE END OF THE THREE-MONTH SHORTENED STATUTORY PERIOD, THEN THE SHORTENED STATUTORY PERIOD WILL EXPIRE ON THE DATE THE ADVISORY ACTION IS MAILED, AND ANY EXTENSION FEE PURSUANT TO 37 C.F.R. 1.136(a) WILL BE CALCULATED FROM THE MAILING DATE OF THE ADVISORY ACTION. IN NO EVENT WILL THE STATUTORY PERIOD FOR RESPONSE EXPIRE LATER THAN SIX MONTHS FROM THE DATE OF THIS FINAL ACTION.

15. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Peter J. Reddig whose telephone number is (571) 272-9031. The examiner can normally be reached on M-F 8:30 a.m.-5:00 p.m..

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Shanon Foley can be reached on (571) 272-0890. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

  
SUSAN UNGAR, PH.D  
PRIMARY EXAMINER

Art Unit: 1642

*Signature on previous page*

Peter J. Reddig, Ph.D.  
Examiner  
Art Unit 1642

PJR

# SCORE Search Results Details for Application 10715066 and Search Result 20060605\_161408\_us- 10-715-066-4\_copy\_500\_1000.rge.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10715066 and Search Result 20060605\_161408\_us-10-715-066-4\_copy\_500\_1000.rge.

[start](#) | [next page](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 10:09:27 ; Search time 3341 Seconds.  
(without alignments)  
9589.242 Million cell updates/sec

Title: US-10-715-066-4\_COPY\_500\_1000  
Perfect score: 501  
Sequence: 1 aaagaaccagcccatcgctg.....aaccactggatatcccttct 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Db	500	AAAGAACCAGCCCATCGCTGAGTCCCAGGTCAATGGAATCCCTCTAGGAACTACCCTG	559
Qy	61	CTACAAGCATGGTTTCAGGATTGAGTTCCCCAAGGACCAGGACCAGTTCCACAGAAGGAA	120
Db	560	CTACAAGCATGGTTTCAGGATTGAGTTCCCCAAGGACCAGGACCAGTTCCACAGAAGGAA	619
Qy	121	ATTTTACCAAAGAAGCATCTACATACACACTCACTGTAGAGACCACAAGTGGCCCAGTCA	180
Db	620	ATTTTACCAAAGAAGCATCTACATACACACTCACTGTAGAGACCACAAGTGGCCCAGTCA	679
Qy	181	CTGAGAAGTACACAGTCCCCACTGAGACCTCAACAACTGAAGGTGACAGCACAGAGACCC	240
Db	680	CTGAGAAGTACACAGTCCCCACTGAGACCTCAACAACTGAAGGTGACAGCACAGAGACCC	739
Qy	241	CCTGGGACACAAGATATATTCCTGTAAAAATCACATCTCCAATGAAAAACATTTGCAGATT	300
Db	740	CCTGGGACACAAGATATATTCCTGTAAAAATCACATCTCCAATGAAAAACATTTGCAGATT	799
Qy	301	CAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGACTCCAGCTGAGACCACAGTTACTG	360
Db	800	CAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGACTCCAGCTGAGACCACAGTTACTG	859
Qy	361	ACTCACATACTCCAGGAAGGACAAACCCATCATTGGGACACTTTATTCTTCCTTCCTTG	420
Db	860	ACTCACATACTCCAGGAAGGACAAACCCATCATTGGGACACTTTATTCTTCCTTCCTTG	919
Qy	421	ACCTATCACCTAAAGGGACCCCAAATTCCAGAGGTGAAACAAGCCTGGAAGTATTCTAT	480
Db	920	ACCTATCACCTAAAGGGACCCCAAATTCCAGAGGTGAAACAAGCCTGGAAGTATTCTAT	979
Qy	481	CAACCACTGGATATCCCTTCT	501
Db	980	CAACCACTGGATATCCCTTCT	1000

# RESULT 5

AC016584/c

LOCUS AC016584 132457 bp DNA linear PRI 29-MAY-2002

DEFINITION Homo sapiens chromosome 19 clone CTD-2596015, complete sequence.

ACCESSION AC016584

VERSION AC016584.5 GI:21240686

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 132457)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 132457)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 132457)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (29-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On May 29, 2002 this sequence version replaced gi:12965319.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.7% of Sequence;  
Estimated Total Number of Errors is 0.3.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 138.1kb). It is clipped at the overlap with AC011464.  
The number of bases overlapped is 14325.

FEATURES                      Location/Qualifiers  
    source                    1. .132457  
                              /organism="Homo sapiens"  
                              /mol\_type="genomic DNA"  
                              /db\_xref="taxon:9606"  
                              /chromosome="19"  
                              /clone="CTD-2596015"

#### ORIGIN

Query Match                      100.0%;    Score 501;    DB 5;    Length 132457;  
Best Local Similarity    100.0%;    Pred. No. 2.8e-161;  
Matches 501;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

```
Qy      1 AAAGAACCAGCCCATCGCTGAGTCCCAGGTCAATGGAAGTCCCTCTAGGAACTACCTG 60
          |||
Db      29314 AAAGAACCAGCCCATCGCTGAGTCCCAGGTCAATGGAAGTCCCTCTAGGAACTACCTG 29255

Qy      61 CTACAAGCATGGTTTCAGGATTGAGTCCCAAGGACCAGGACCAGTTCACAGAAGGAA 120
          |||
Db      29254 CTACAAGCATGGTTTCAGGATTGAGTCCCAAGGACCAGGACCAGTTCACAGAAGGAA 29195

Qy      121 ATTTTACCAAAGAAGCATCTACATACACACTCACTGTAGAGACCACAAGTGGCCAGTCA 180
          |||
Db      29194 ATTTTACCAAAGAAGCATCTACATACACACTCACTGTAGAGACCACAAGTGGCCAGTCA 29135

Qy      181 CTGAGAAGTACACAGTCCCCACTGAGACCTCAACAAGTGAAGGTGACAGCACAGAGACCC 240
          |||
Db      29134 CTGAGAAGTACACAGTCCCCACTGAGACCTCAACAAGTGAAGGTGACAGCACAGAGACCC 29075

Qy      241 CCTGGGACACAAGATATATTCCTGTAAAAATCACATCTCCAATGAAAACATTTGCAGATT 300
          |||
Db      29074 CCTGGGACACAAGATATATTCCTGTAAAAATCACATCTCCAATGAAAACATTTGCAGATT 29015

Qy      301 CAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGACTCCAGCTGAGACCACAGTTACTG 360
          |||
Db      29014 CAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGACTCCAGCTGAGACCACAGTTACTG 28955

Qy      361 ACTCACATACTCCAGGAAGGACAAACCCATCATTTGGGACACTTTATTCTTCCTTCCTTG 420
          |||
Db      28954 ACTCACATACTCCAGGAAGGACAAACCCATCATTTGGGACACTTTATTCTTCCTTCCTTG 28895

Qy      421 ACCTATCACCTAAAGGGACCCCAAATTCAGAGGTGAAACAAGCCTGGAAGTATTCTAT 480
          |||
Db      28894 ACCTATCACCTAAAGGGACCCCAAATTCAGAGGTGAAACAAGCCTGGAAGTATTCTAT 28835

Qy      481 CAACCACTGGATATCCCTTCT 501
          |||
Db      28834 CAACCACTGGATATCCCTTCT 28814
```

#### RESULT 6

AC166942

LOCUS                      AC166942                      247108 bp                      DNA                      linear                      HTG 23-JAN-2006

DEFINITION                      Bos taurus clone CH240-121L8, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 30  
                              unordered pieces.

ACCESSION                      AC166942

VERSION                      AC166942.2    GI:85665651

KEYWORDS                      HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

SOURCE                      Bos taurus (cattle)

ORGANISM                      Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 247108)  
AUTHORS Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,  
Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,  
Beraducci,A., Biswalo,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,  
Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I.,  
Chacko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G., Chen,R.,  
Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A.,  
Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De  
Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H.,

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006
---------------------------------



## Sequence Revision History

[PubMed](#)[Nucleotide](#)[Protein](#)[Genome](#)[Structure](#)[PMC](#)[Taxonomy](#)[OMIM](#)[Books](#)

Find (Accessions, GI numbers or Fasta style SeqIds)

[About Entrez](#)

difference between I and II as

[Entrez](#)

### Revision history for AC016584

#### Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

[Help|FAQ](#)

Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

GI	Version	Update Date	Status	I	II
21240686	5	<a href="#">May 29 2002 7:29 AM</a>	Live	<input checked="" type="radio"/>	<input type="radio"/>
12965319	4	<a href="#">Feb 20 2001 4:55 AM</a>	Dead	<input type="radio"/>	<input checked="" type="radio"/>
9211207	3	<a href="#">Jul 15 2000 4:53 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
6758722	2	<a href="#">Mar 3 2000 5:46 PM</a>	Dead	<input type="radio"/>	<input type="radio"/>
6758722	2	<a href="#">Jan 26 2000 6:08 PM</a>	Dead	<input type="radio"/>	<input type="radio"/>
6524122	1	<a href="#">Dec 4 1999 6:04 PM</a>	Dead	<input type="radio"/>	<input type="radio"/>

Accession AC016584 was first seen at NCBI on Dec 4 1999 6:04 PM

[Check sequence revision history](#)[How to create WWW links to Entrez](#)[LinkOut](#)[My NCBI \(Cubby\)](#)

#### Related resources

[BLAST](#)[Reference sequence project](#)[LocusLink](#)[Clusters of orthologous groups](#)[Protein reviews on the web](#)

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)





## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

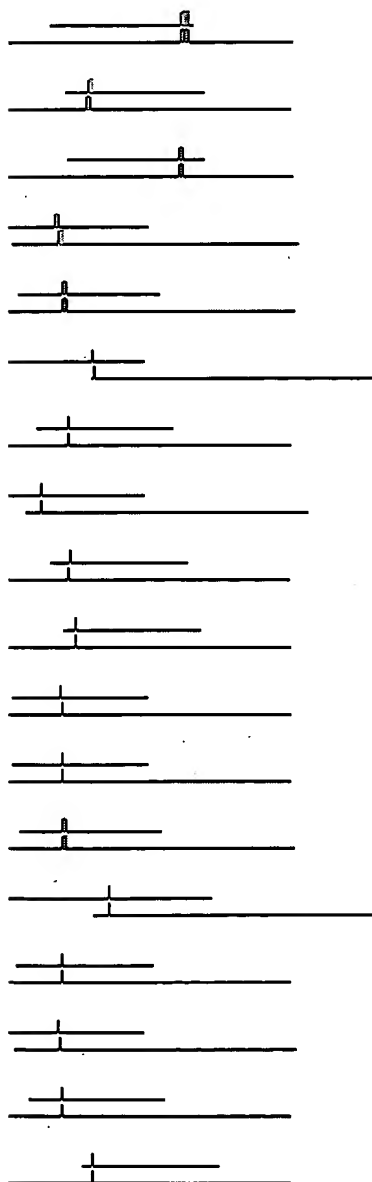
### BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.15 [Oct-15-2006]

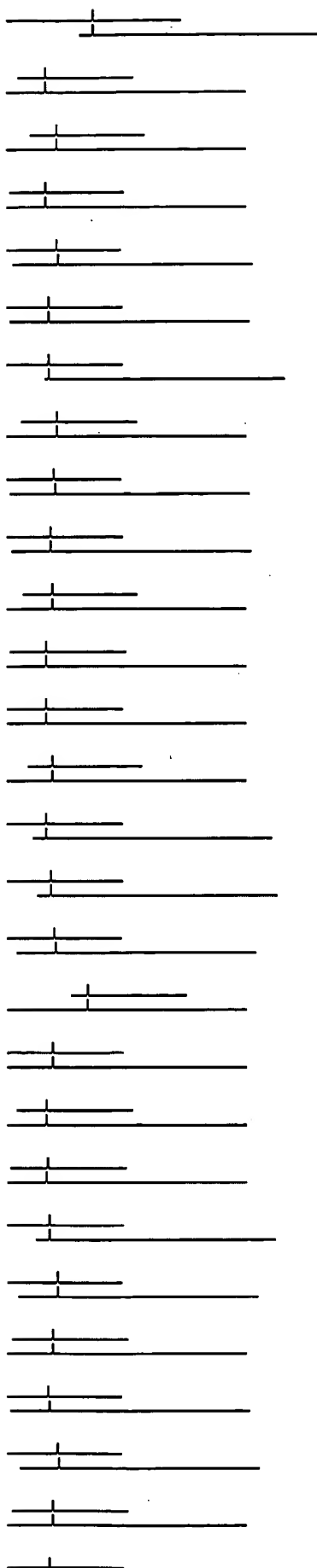
Match:  Mismatch:  gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☒ View option Masking character option  Masking color option ☐ Show CDS translation **Sequence 1:** gi|24419040|gb|AF414442.2| = *SEQ ID NO: 4*

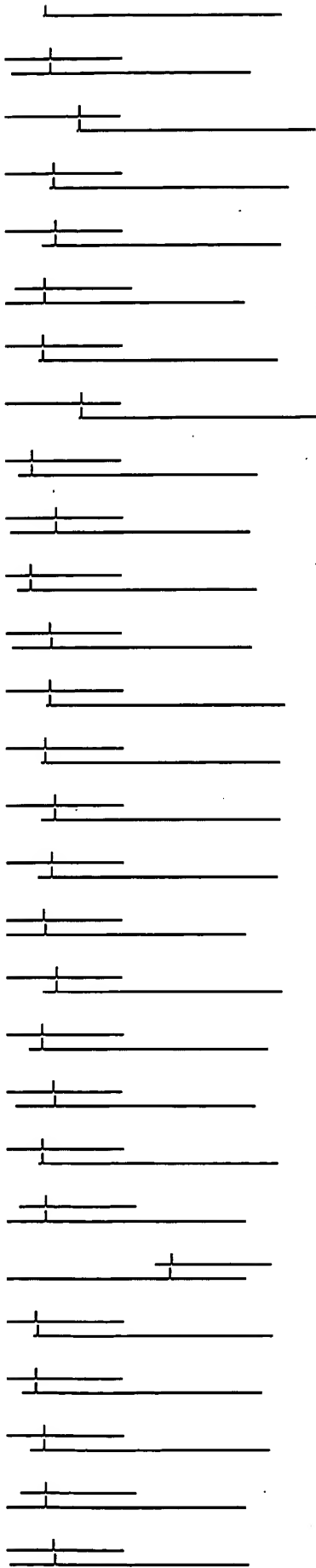
Length = 66765 (1 .. 66765)

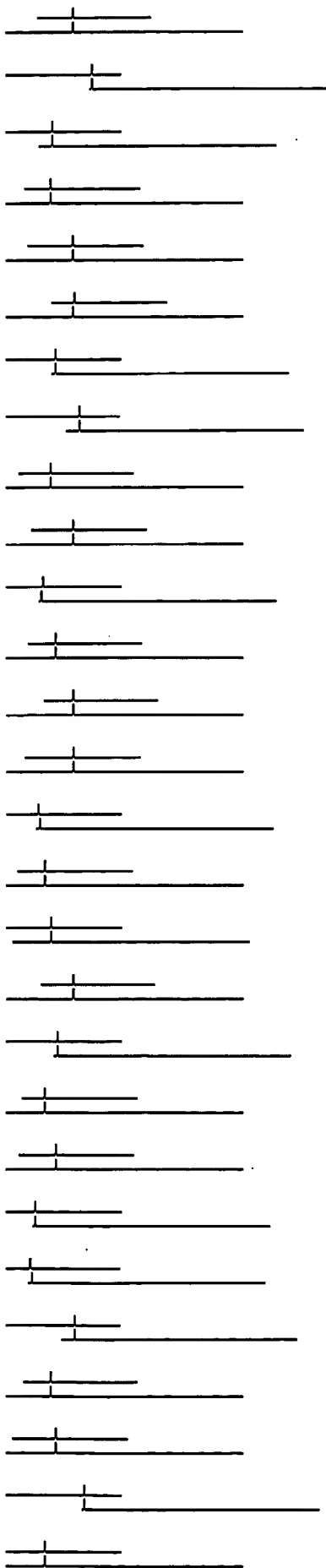
**Sequence 2:** gi|6758722|gb|AC016584.2|AC016584

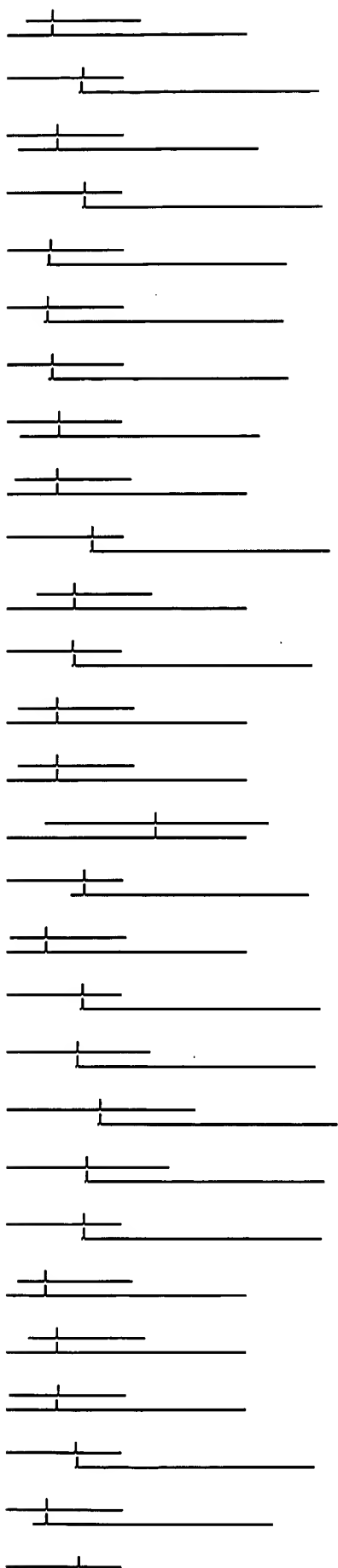
Length = 137536 (1 .. 137536)

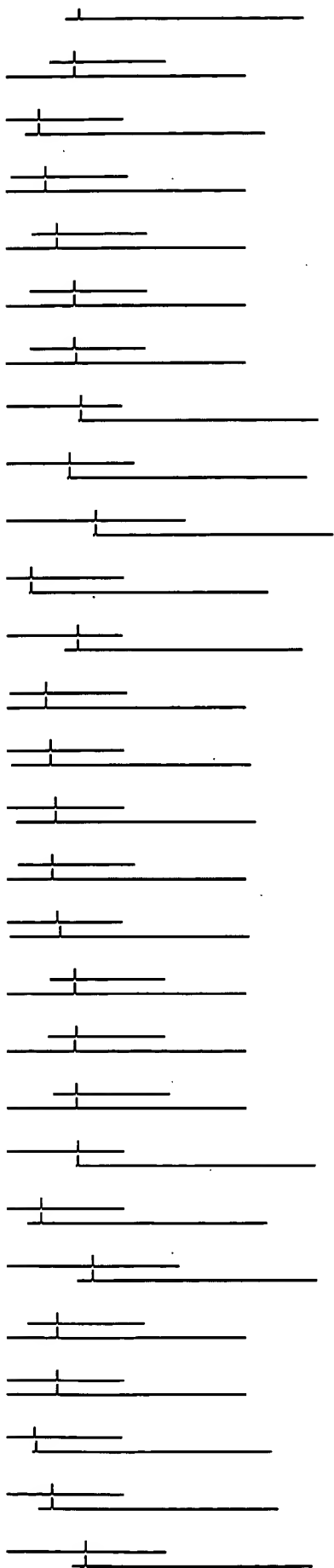












—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—

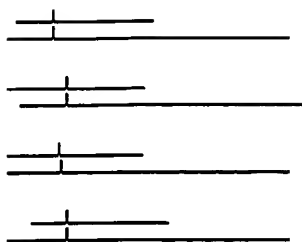
—+—  
—

—+—  
—

—+—  
—

—+—  
—

—+—  
—



1

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



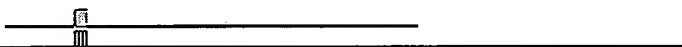
Score = 3694 bits (1921), Expect = 0.0  
Identities = 1935/1937 (99%), Gaps = 2/1937 (0%)  
Strand=Plus/Minus

Query	597	CAGGACCAGTTCCACAGAAGGAAATTTTACCAAAGAAGCATCTACATACACACTCACTGT	656
Sbjct	86743	CAGGACCAGTTCCACAGAAGGAA-TTTTACCAAAGAAGCATCTACATACACACTCACTGT	86685
Query	657	AGAGACCACAAGTGGCCAGTCACTGAGAAGTACACAGTCCCCACTGAGACCTCAACAAC	716
Sbjct	86684	AGAGACCACAAGTGGCCAGTCACTGAGAAGTACACAGTCCCCACTGAGACCTCAACAAC	86625
Query	717	TGAAGGTGACAGCACAGAGACCCCCTGGGACACAAGATATATTCCTGTAAAAATCACATC	776
Sbjct	86624	TGAAGGTGACAGCACAGAGACCCCCTGGGACACAAGATATATTCCTGTAAAAATCACATC	86565
Query	777	TCCAATGAAAACATTTGCAGATTCAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGAC	836
Sbjct	86564	TCCAATGAAAACATTTGCAGATTCAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGAC	86505
Query	837	TCCAGCTGAGACCACAGTTACTGACTCACATACTCCAGGAAGGACAAACCCATCATTGG	896
Sbjct	86504	TCCAGCTGAGACCACAGTTACTGACTCACATACTCCAGGAAGGACAAACCCATCATTGG	86445
Query	897	GACACTTTATTCTTCCTTCCTTGACCTATCACCTAAAGGGACCCCAAATTCAGAGGTGA	956
Sbjct	86444	GACACTTTATTCTTCCTTCCTTGACCTATCACCTAAAGGGACCCCAAATTCAGAGGTGA	86385
Query	957	AACAAGCCTGGAAGTATTCTATCAACCACTGGATATCCCTTCTCCTCTCCTGAACCTGG	1016
Sbjct	86384	AACAAGCCTGGAAGTATTCTATCAACCACTGGATATCCCTTCTCCTCTCCTGAACCTGG	86325
Query	1017	CTCTGCAGGACACAGCAGAATAAGTACCAGTGCGCCTTTGTGTCATCATCTGCTTCAGTTCT	1076
Sbjct	86324	CTCTGCAGGACACAGCAGAATAAGTACCAGTGCGCCTTTGTGTCATCATCTGCTTCAGTTCT	86265
Query	1077	CGATAATAAAATATCAGAGACCAGCATATTCTCAGGCCAGAGTCTCACCTCCCCTCTGTC	1136
Sbjct	86264	CGATAATAAAATATCAGAGACCAGCATATTCTCAGGCCAGAGTCTCACCTCCCCTCTGTC	86205
Query	1137	TCCTGGGGTGCCCGAGGCCAGAGCCAGCACAATGCCCAAAGTCTCAGCTATCCCTTTTCCAT	1196
Sbjct	86204	TCCTGGGGTGCCCGAGGCCAGAGCCAGCACAATGCCCAAAGTCTCAGCTATCCCTTTTCCAT	86145
Query	1197	GACACTAAGCAATGCAGAAACAAGTGCCGAAAGGGTCAAGACACAATTCCTCTCTGGG	1256



Sbjct	86144	 GACACTAAGCAATGCAGAAACAAGTGCCGAAAGGGTCAGAAGCACAAATTTCTCTCTGGG	86085
Query	1257	GACTCCATCAATATCCACAAAGCAGACAGCAGAGACTATCCTTACCTTCCATGCCTTCGC	1316
Sbjct	86084	 GACTCCATCAATATCCACAAAGCAGACAGCAGAGACTATCCTTACCTTCCATGCCTTCGC	86025
Query	1317	TGAGACCATGGATATACCCAGCACCCACATAGCCAAGACTTTGGCTTCAGAATGGTTGGG	1376
Sbjct	86024	 TGAGACCATGGATATACCCAGCACCCACATAGCCAAGACTT-GGCTTCAGAATGGTTGGG	85966
Query	1377	AAGTCCAGGTACCCTTGGTGGCACCAGCACTTCAGCGCTGACAACCACATCTCCATCTAC	1436
Sbjct	85965	 AAGTCCAGGTACCCTTGGTGGCACCAGCACTTCAGCGCTGACAACCACATCTCCATCTAC	85906
Query	1437	CACTTTAGTCTCAGAGGAGACCAACACCCATCACTCCACGAGTGGAAAGGAAACAGAAGG	1496
Sbjct	85905	 CACTTTAGTCTCAGAGGAGACCAACACCCATCACTCCACGAGTGGAAAGGAAACAGAAGG	85846
Query	1497	AACTTTGAATACATCTATGACTCCACTTGAGACCTCTGCTCCTGGAGAAGAGTCCGAAAT	1556
Sbjct	85845	 AACTTTGAATACATCTATGACTCCACTTGAGACCTCTGCTCCTGGAGAAGAGTCCGAAAT	85786
Query	1557	GACTGCCACCTTGGTCCCCACTCTAGGTTTTACAACCTTTGACAGCAAGATCAGAAGTCC	1616
Sbjct	85785	 GACTGCCACCTTGGTCCCCACTCTAGGTTTTACAACCTTTGACAGCAAGATCAGAAGTCC	85726
Query	1617	ATCTCAGGTCTCTTCATCCCACCCAACAAGAGAGCTCAGAACCACAGGCAGCACCTCTGG	1676
Sbjct	85725	 ATCTCAGGTCTCTTCATCCCACCCAACAAGAGAGCTCAGAACCACAGGCAGCACCTCTGG	85666
Query	1677	GAGGCAGAGTTCCAGCACAGCTGCCCACGGGAGCTCTGACATCCTGAGGGCAACCACTTC	1736
Sbjct	85665	 GAGGCAGAGTTCCAGCACAGCTGCCCACGGGAGCTCTGACATCCTGAGGGCAACCACTTC	85606
Query	1737	CAGCACCTCAAAAGCATCATCATGGACCAGTGAAAGCACAGCTCAGCAATTTAGTGAACC	1796
Sbjct	85605	 CAGCACCTCAAAAGCATCATCATGGACCAGTGAAAGCACAGCTCAGCAATTTAGTGAACC	85546
Query	1797	CCAGCACACACAGTGGGTGGAGACAAGTCCTAGCATGAAAACAGAGAGACCCCCAGCATC	1856
Sbjct	85545	 CCAGCACACACAGTGGGTGGAGACAAGTCCTAGCATGAAAACAGAGAGACCCCCAGCATC	85486
Query	1857	AACCAGTGTGGCAGCCCCATACCACTTCTGTTCCTCAGTGGTCTCTGGCTTCACCAC	1916
Sbjct	85485	 AACCAGTGTGGCAGCCCCATACCACTTCTGTTCCTCAGTGGTCTCTGGCTTCACCAC	85426
Query	1917	CCTGAAGACCAGCTCCACAAAAGGGATTTGGCTTGAAGAAACATCTGCAGACACACTCAT	1976
Sbjct	85425	 CCTGAAGACCAGCTCCACAAAAGGGATTTGGCTTGAAGAAACATCTGCAGACACACTCAT	85366
Query	1977	CGGAGAATCCACAGCTGGCCCAACCACCCATCAGTTTGCTGTTCCCACTGGGATTTCAAT	2036
Sbjct	85365	 CGGAGAATCCACAGCTGGCCCAACCACCCATCAGTTTGCTGTTCCCACTGGGATTTCAAT	85306
Query	2037	GACAGGAGGCAGCAGCACCAGGGGAAGCCAGGGCACAACCCACCTACTCACCAGAGCCAC	2096
Sbjct	85305	 GACAGGAGGCAGCAGCACCAGGGGAAGCCAGGGCACAACCCACCTACTCACCAGAGCCAC	85246
Query	2097	AGCATCATCTGAGACATCCGAGATTTGACTCTGGCCACGAACGGTGTCCAGTCTCCGT	2156
Sbjct	85245	 AGCATCATCTGAGACATCCGAGATTTGACTCTGGCCACGAACGGTGTCCAGTCTCCGT	85186
Query	2157	GTCTCCAGCAGTGAGCAAGACGGCTGCTGGCTCAAGTCCTCCAGGAGGGACAAAGCCATC	2216
Sbjct	85185	 GTCTCCAGCAGTGAGCAAGACGGCTGCTGGCTCAAGTCCTCCAGGAGGGACAAAGCCATC	85126

Query	2217	ATATACAATGGTTTCTTCTGTCCCTGAGACATCATCTCTACAGTCCTCAGCTTTCAG	2276
Sbjct	85125	ATATACAATGGTTTCTTCTGTCCCTGAGACATCATCTCTACAGTCCTCAGCTTTCAG	85066
Query	2277	GGAAGGAACCAGCCTGGGACTGACTCCATTAAACACTAGACATCCCTTCTTCCCCTGA	2336
Sbjct	85065	GGAAGGAACCAGCCTGGGACTGACTCCATTAAACACTAGACATCCCTTCTTCCCCTGA	85006
Query	2337	ACCAGACTCTGCAGGACACACCAAGATAAGCACCAGCATTCTCTGTTGTCATCTGCTTC	2396
Sbjct	85005	ACCAGACTCTGCAGGACACACCAAGATAAGCACCAGCATTCTCTGTTGTCATCTGCTTC	84946
Query	2397	AGTTCTTGAGGATAAAGTGTGAGCGACCAGCACATTCTCACACCACAAAGCCACCTCATC	2456
Sbjct	84945	AGTTCTTGAGGATAAAGTGTGAGCGACCAGCACATTCTCACACCACAAAGCCACCTCATC	84886
Query	2457	TATTACCACAGGGACTCCTGAAATCTCAACAAAGACAAAGCCCAGCTCAGCCGTTCTTTC	2516
Sbjct	84885	TATTACCACAGGGACTCCTGAAATCTCAACAAAGACAAAGCCCAGCTCAGCCGTTCTTTC	84826
Query	2517	CTCCATGACCCTAAGCA	2533
Sbjct	84825	CTCCATGACCCTAAGCA	84809



Score = 2488 bits (1294), Expect = 0.0  
 Identities = 1347/1361 (98%), Gaps = 5/1361 (0%)  
 Strand=Plus/Plus

Query	11589	GAGCTCTGGAGTTACTTTTCAAGACCAGATCCCACAAGCAAAAAGGCAGAGCAGACTTC	11648
Sbjct	38757	GAGCTCTGGAGTTACTTTTCAAGACCAGATCCCACAAGCAAAAAGGCAGAGCAGACTTC	38816
Query	11649	CACTCAGCTTCCCACCACCACTTCTGCACATCCAGGGCAGGTGCCAGATCAGCAGCAAC	11708
Sbjct	38817	CACTCAGCTTCCCACCACCACTTCTGCACATCCAGAGCAGGTGCCAGATCAGCAGCAAC	38876
Query	11709	AACTCTGGATGTGATCCACACACAGCAAAACTCCAGATGCAACTTTTCAGAGACAAGG	11768
Sbjct	38877	AACTCTGGATGTGATCCACACACAGCAAAACTCCAGATGCAACTTTTCAGAGACAAGG	38936
Query	11769	GCAGACAGCTCTTACAACAGAGGCAAGAGCTACATCTGACTCCTGGAATGAGAAAGAAAA	11828
Sbjct	38937	GCAGACAGCTCTTACAACAGAGGCAAGAGCTACATCTGACTCCTGGAATGAGAAAGAAAA	38996
Query	11829	ATCAACCCCAAGTGCACCTTGGATCACTGAGATGATGAATTCTGTCTCAGAAGATACCAT	11888
Sbjct	38997	ATCAACCCCAAGTGCACCTTGGATCACTGAGATGATGAATTCTGTCTCAGAAGATACCAT	39056
Query	11889	CAAGGAGGTTACCAGCTCCTCCAGTGTATTAAAGGACCCTGAATACGCTGGACATAAACT	11948
Sbjct	39057	CAAGGAGGTTACCAGCTCCTCCAGTGTGTTAA-GGACCCTGAATACGCTGGACATAAACT	39115
Query	11949	TGGAATCTGGGACGACTTCATCCCCAAGTTTGGAAGAGCAGCCCATATGAGAGAGTTGCC	12008
Sbjct	39116	TGGAATCTGGGACGACTTCATCCCCAAGTT-GGAAAAGCAGCCCATATGAGAGAATTGCC	39174
Query	12009	CCTTCTGAGTCCACCACAGGACAAAGAGGCAATTACCCCTTCTACAAACACAGTAGAGAC	12068
Sbjct	39175	CCTTCTGAGTCTACCACAG-ACAAAGAGGCAATTACCCCTTCTACAAACACAGTAGAGAC	39233

Query	12069	CACAGGCTGGGTCAACAAGTTCCGAACATGCTTCTCATTCCACTATCCCAGCCCACTCAGC	12128
Sbjct	39234	CACTGGCTGGGTCAACAAGTTCCGAACATGCTTCTCATTCCACTATCCCAGCCCACTCAGC	39293
Query	12129	GTCATCCAAACTCACATCTCCAGTGGTTACAACCTCCACCAGGGAACAAGCAATAGTTTC	12188
Sbjct	39294	GTCATCCAAACTCACATCTCCAGTGGTTACAACCTCCACCAGGGAACAAGCAATAGTTTC	39353
Query	12189	TATGTCAACAACCACATGGCCAGAGTCTACAAGGGCTAGAACAGAGCCTAATTCCTTCTT	12248
Sbjct	39354	TATGTCAACAACCACATGGCCAGAGTCTACAAGGGCTAGAACAGAGCCTAATTCCTTCTT	39413
Query	12249	GACTATTGAACTGAGGGACGTCAGCCCTTACATGGACACCAGCTCAACCACACAAACAAG	12308
Sbjct	39414	GACTATTGAACTGAGGGACGTCAGCCCTTACATGGACACCAGCTCAACCACACAAACAAG	39473
Query	12309	TATTATCTCTTCCCCAGGTTCCACTGCGATACCAAGGGGCCTAGAACAGAAATTACCTC	12368
Sbjct	39474	T-TTATCTCTTCCCCAGGTTCCACTGCGATACCAAGGGGCCTAGAACAGAAATTACCTC	39532
Query	12369	CTCTAAGAGAATATCCAGCTCATTCTTGCCAGTCTATGAGGTCGTCAGACAGCCCCTC	12428
Sbjct	39533	CTCTAAGAGAATATCCAGCTCATTCTTGCCAGTCTATGAGGTCGTCAGACAGCCCCTC	39592
Query	12429	AGAAGCCATCACCAGGCTGTCTAACTTTCCTGCCATGACAGAATCTGGAGGAATGATCCT	12488
Sbjct	39593	AGAAGCCATCTCCAGGCTGTCTAACTTTCCTGCCATGACAGAATCTGGAGGAATGATCCT	39652
Query	12489	TGCTATGCAAACAAGTCCACCTGGCGCTACATCACTAAGTGCACCTACTTTGGATACATC	12548
Sbjct	39653	TGCTATGCAAACAAGTCCACCTGGCGCTACATCACTAAGTGCACCTACTTTGGATACATC	39712
Query	12549	AGCCACAGCCTCCTGGACAGGGACTCCACTGGCTACGACTCAGAGATTACATACTCAGA	12608
Sbjct	39713	AGCCACAGCCTCCTGGACAGGGACTCCACTGGCTACGACTCAGAGATTACATACTCAGA	39772
Query	12609	GAAGACCACTCTCTTTAGCAAAGGTCCTGAGGATACATCACAGCCAAGCCCTCCCTCTGT	12668
Sbjct	39773	GAAGACCACTCTCTTTAGCAAAGGTCCTGAGGATACATCACAGCCAAGCCCTCCCTCTGT	39832
Query	12669	GGAAGAAACCAGCTCTTCCTCTTCCCTGGTACCTATCCATGCTACAACCTCGCCTTCCAA	12728
Sbjct	39833	GGAAGAAACCAGCTCTTCCTCTTCCCTGGTACCTATCAATGCTACAACCTCGCCTTCCAA	39892
Query	12729	TATTTTGTGACATCACAAGGGCACAGTCCCTCCTCTACTCCACCTGTGACCTCAGTTTT	12788
Sbjct	39893	TATTTTGTGACATCACAAGGGCACAGTCCCTCCTCTACTCCACCTGTGACCTCAGTTTT	39952
Query	12789	CTTGTCTGAGACCTCTGGCCTGGGGAAGACCACAGACATGTCGAGGATAAGCTTGGAACC	12848
Sbjct	39953	CTTGTCTGAGACCTCTGGCCTGGGGAAGACCACAGACATGTCGAGGATAAGCTTGGAACC	40012
Query	12849	TGGCACAAGTTTACCTCCCAATTTGAGCAGTACAGCAGGTGAGGCGTTATCCACTTATGA	12908
Sbjct	40013	TGGCACAAGTTTACCTCCCAATTTGAGCACTACAGCAGGTGAGGCGTTATCCACTTATGA	40072
Query	12909	AGCCTCCAGAGATACAAAGGCAATTCATCATTCTGCAGACA	12949
Sbjct	40073	AGCCTCCAGAGATACAAA-GCAATTCATCATTCTACAGACA	40112

Score = 2207 bits (1148), Expect = 0.0  
Identities = 1194/1210 (98%), Gaps = 5/1210 (0%)  
Strand=Plus/Minus

Query	10333	CCAAACTCTGTGAGCTCATTGACAGATAAATCCAAACATAAAACCGAGACATGGGTAAGC	10392
Sbjct	84780	CCAAACTCTGTGAGCTCATTGACAGATATATCCAAACATAAAACCGAGACATGGGTGAGC	84721
Query	10393	ACCACAGCCATTCCCTCCACTGTCCTGAATAATAAGATAATGGCAGCTGAACAACAGACA	10452
Sbjct	84720	ACCACAGCCATTCCCTCCACTGTCCTGAATAATAAGATAATGGCAGCTGAACAACAGACA	84661
Query	10453	AGTCGATCTGTGGATGAGGCTTATTTCATCAACTAGTTCTTGGTCAGATCAGACATCTGGG	10512
Sbjct	84660	AGTCGATCTGTGGATGAGGCTTATTTCATCAACTAGTTCTTGGTCAGATCAGACATCTGGG	84601
Query	10513	AGTGACATCACCCCTTGGTGCATCTCCTGATGTCACAAACACATTATACATCACCTCCACA	10572
Sbjct	84600	AGTGACATCACCCCTTGGTGCATCTCCTGATGTCACAAACACATTATACATCACCTCCACA	84541
Query	10573	GCACAAACCACCTCACTAGTGTCTCTGCCCTCTGGAGACCAAGGCATTACAAGCCTCACC	10632
Sbjct	84540	GCACAAACCACCTCACTAGTATCTCTGCCCTCTGGAGACCAAGGCATTACAAGCCTCACC	84481
Query	10633	AATCCCTCAGGAGGAAAAACAAGCTCTGCGTCATCTGTACATCTCCTTCAATAGGGCTT	10692
Sbjct	84480	AATCCCTCAGGAGGAAAAACAAGCTCTGCATCATCTGTACATCTCCTTCAATAGGGCTT	84421
Query	10693	GAGACTCTGAGGGCCAATGTAAGTGCAGTGAAAAGTGACATTGCCCTACTGCTGGGCAT	10752
Sbjct	84420	GAGACTCTGATGGCCAATGTAAGTGCAGTGACAAGTGACATTGCCCTACTGCTGGGCAT	84361
Query	10753	CTATCTCAGACTTCATCTCCTGCGGAAGTGAGCATCCTGGACGTAACCACAGCTCCTACT	10812
Sbjct	84360	CTATCTCAGACTTCATCTCCTGCGGAAGTGAGCATCCTGGACATAACCACAGCTCCTACT	84301
Query	10813	CCAGGTATCTCCACCACCATCACCACCATGGGAACCAACTCAATCTCAACTACCACACCC	10872
Sbjct	84300	CCAGGTATCTCCACCACCATCACCACCATGGGAACCAACTCAATCTCAACTACCACACCC	84241
Query	10873	AACCCAGAAGTGGGTATGAGTACCATGGACAGACCCCCGGCCACAGAGAGGCGCACAACT	10932
Sbjct	84240	AACCCAGAAGTGGGTATGAGTACCATGGACAGACCCCCGGCCACAGAGAGGCGCACAACT	84181
Query	10933	TCTACAGAACACCCTTCCACCTGGTCTTCCACAGCTGCATCAGATTCTGGACTGTCACA	10992
Sbjct	84180	TCTACAGAACACCCTTCCACCTGGTCTTCCACAGCTGCATCAGATTCTGGACTGTCACA	84121
Query	10993	GACATGACTTCAAACCTTGAAAGTTGCAAGATCTCCTGGAACAATTTCCACAATGCATACA	11052
Sbjct	84120	GACATGACTTCAAACCTTGAAAGTTGCAAGATCTCCTGGAACAATTTCCACAATGCATACA	84061
Query	11053	ACTTCATTCTTAGCCTCAAGCACTGAATTAGACTCCATGTCTACTCCCCATGGCCGTATA	11112
Sbjct	84060	ACTTCATTCTTAGCCTCAAGCACTGAATTAGACTCCATGTCTACTCCCCATGGCCGTATA	84001
Query	11113	ACTGTCATTGGAACCAAGCCTGGTCACTCCATCCTCTGATGCTTCAGCTGTAAAGACAGAG	11172
Sbjct	84000	ACTGTCATTGGAACCAAGCCTGGTCACTCCATCCTCTGATGCTTCAGCTGTAAAGACAGAG	83941
Query	11173	ACCAGTACAAGTGAAAGAACATTGAGTCCTTCAGACACAACCTGCATCTACTCCCATCTCA	11232
Sbjct	83940	ACCAGTACAAGTGAAAGAACATTGAGTCCTTCAGACACAACCTGCATCTACTCCCATCTCA	83881
Query	11233	ACTTTTTCTCGTGTCCAGAGGATGAGCATCTCAGTTCCTGACATTTTAAGTACAAGTTGG	11292

Sbjct	83880		ACTTTTTCTCGTGTCAGAGGATGAGCATCTCAGTTCCTGACATTTTAAGTACAAGTTGG	83821
Query	11293		ACTCCAGTAGTACAGAAGCAGAAGATGTGCCTGTTTCAATGGTTTCTACAGATCATGCT	11352
Sbjct	83820		ACTCCAGTAGTACAGAAGCAGAAGATGTGCCTGTTTCAATGGTTTCTACAGATCATGCT	83761
Query	11353		AGTACAAAGACTGACCCAAATACGCCCCGTGCCACTTTTCTGTTTGATTCTCTGT---CC	11409
Sbjct	83760		AGTACAAAGACTGACCCAAATATGCCCCGTGCCACTTTTCTGTTTGATTCTCTGTTCANC	83701
Query	11410		ACTCTTG-AC-TGGGACACTGGGAGATCTCTGTCTATCAGCCACAGCCACTACCTCAGCTC	11467
Sbjct	83700		ACTCTTGACATGGGACACTGGGAGATCTCTGTCTATCAGCCACAGCCACTACCTCAGCTC	83641
Query	11468		CTCAGGGGGCCACAACCTCCCCAGGAACCTCACTTTGGAAACCATGATCAGCCCAGCTACCT	11527
Sbjct	83640		CTCAGGGGGCCACAACCTCCCCAAGAACCTCACTTTGGAAACCATGATCAGCCCAGCTACCT	83581
Query	11528		CACAGTTGCC 11537	
Sbjct	83580		CACAGTTGCC 83571	

---

Score = 1302 bits (677), Expect = 0.0  
Identities = 728/739 (98%), Gaps = 3/739 (0%)  
Strand=Plus/Plus

Query	23289		ACCTGCCGTGACCTCACCTCATCTGTTCACCCACATTCTAGCACATATnnnnnnnnTC	23348
Sbjct	22545		ACCTGCCGTGACCTCACCTCATCTGTTCACCCACATTCTAGCACATATCCCCCCTC	22603
Query	23349		TCCCCTTCCTGTGACTTCACTTCTCACCTCTGGCCCGGCGACAACCACAGATATCTTGGG	23408
Sbjct	22604		TCCCCTTCCTGTGACTTCACTTCTCACCTCTGGCCCGGCGACAACCACAGATATCTTGGG	22663
Query	23409		TACAAGCACAGAACCTGGAACCACTTCACTTCAAGTTTGAGCACCACCTCCCATGAGAG	23468
Sbjct	22664		TACAAGCACAGAACCTGGAACCACTTCACTTCAAGTTTGAGCACCACCTCCCATGAGAG	22723
Query	23469		ACTGACCACTTACAAAGACACTGCACATACAGAAGCCGTGCATCCTTCCACAAACACAGG	23528
Sbjct	22724		ACTGACCACTTACAAAGACACTGCACATACAGAAGCCGTGCATCCTTCCACAAACACAGG	22783
Query	23529		AGGGACCAATGTGGCAACCACAGCTCTGGATATAAATCACAGTCCTCTGTCTAGCTGA	23588
Sbjct	22784		AGGGACCAATGTGGCAACCACAGCTCTGGATATAAATCACAGTCCTCTGTCTAGCTGA	22843
Query	23589		CTCATCTCCAATGTGTACCACCTCCACCATGGGGGATACAAGTGTCTCACATCAACTCC	23648
Sbjct	22844		CTCATCTCCAATGTGTACCACCTCCACCATGGGGGATACAAGTGTCTCACATCAACTCC	22903
Query	23649		TGCCTTCCTTGAGACTAGGAGGATTAGACAGAGCTAGCTTCCTCCCTGACCCCTGGATT	23708
Sbjct	22904		TGCCTTCCTTGAGACTAGGAGGATTAGACAGAGCTAGCTTCCTCCCTGACCCCTGGATT	22963
Query	23709		GAGGGAGTCCAGTGGCTCTGAAGGGACCAGCTCAGGCACCAAGATGAGCACTGTCTCTC	23768
Sbjct	22964		GAGGGAGTCCAGTGGCTCTGAAGGGACCAGCTCAGGCACCAAGATGAGCACTGTCTCTC	23023
Query	23769		TAAAGTGCCCACTGGTGCTACTACTGAGATCTCAAGGAAGACGTACCTCCATCCCAGG	23828

Sbjct	23024		TAAAGTGCCCACTGGTGCTACTACTGAGATCTCCAAGGAAGACGTCACCTCCATCCCAGG	23083
Query	23829		TCCCGCTCAATCCACAATATCACCAGACATCTCCACAAGAACCGTCAGCTGGTTCTCTAC	23888
Sbjct	23084		TCCCGCTCAATCCACAATATCACCAGACATCTCCACAAGAACCGTCAGCTGGTTCTCTAC	23143
Query	23889		ATCCCCTGTCATGACAGAATCAGCAGAAATAACCATGAACACCCATACAAGTCCTTTAGG	23948
Sbjct	23144		ATCCCCTGTCATGACAGAATCAGCAGAAATAACCATGAACACCCATACAAGTCCTTTAGG	23203
Query	23949		GGCCACAACACAAGGCACCACTACTTT-GGCCACGTCAAGCACAACCTCTTTGACAATGA	24007
Sbjct	23204		GGCCACAACACAAGGCACCACTACTTTGGGCCACGTCAAGGCACAACCTCTTTGACAATGA	23263
Query	24008		CACA-CTCAACTATATCTC 24025	
Sbjct	23264		CACACCTCCACTATATCTC 23282	

Score = 1190 bits (619), Expect = 0.0  
Identities = 639/644 (99%), Gaps = 2/644 (0%)  
Strand=Plus/Plus

Query	21620		CCACAGACATGTTACACACAAGCCCAGAACTTGTAACCAGTTCACCTCCAAAGCTGAGCC	21679
Sbjct	26180		CCACAGACATGTTACACACAAGCCCAGAACT-GTAACCAGT-CACCTCCAAAGCTGAGCC	26237
Query	21680		ACACTTCAGATGAGAGACTGACCACTGGCAAGGACACCACAAATACAGAAGCTGTGCATC	21739
Sbjct	26238		ACACTTCACATGAGAGACTGACCACTGGCAAGGACACCACAAATACAGAAGCTGTGCATC	26297
Query	21740		CTTCCACAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTTTGGACATGAATCCCCTT	21799
Sbjct	26298		CTTCCACAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTCTGGACATGAATCCCCTT	26357
Query	21800		CCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTACCTCCA	21859
Sbjct	26358		CCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTACCTCCA	26417
Query	21860		CCCAGGAGGATACAACTGTTGCCATATCAACCCCTCACTTCTTGGAGACTAGCAGAATTC	21919
Sbjct	26418		CCCAGGAGGATACAACTGTTGCCATATCAACCCCTCACTTCTTGGAGACTAGCAGAATTC	26477
Query	21920		AGAAAGAGTCAATTTCCCTCCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTGGAGA	21979
Sbjct	26478		AGAAAGAGTCAATTTCCCTCCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTGGAGA	26537
Query	21980		CAAGCTCAGCCATAGAGACAAGTGCTGTCTTTCTGAAGTGTCCATTGGTGCTACTACTG	22039
Sbjct	26538		CAAGCTCAGCCATAGAGACAAGTGCTGTCTTTCTGAAGTGTCCGTTGGTGCTACTACTG	26597
Query	22040		AGATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTGCTGAGT	22099
Sbjct	26598		AGATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTGCTGAGT	26657
Query	22100		CCACAATGTTGCCAGAAATATCCACCACAAGAAAAATCATTAAAGTTCCTACTTCCCCCA	22159
Sbjct	26658		CCACAATGTTGCCAGAAATATCCACCACAAGAAAAATCATTAAAGTTCCTACTTCCCCCA	26717
Query	22160		TCCTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCCTCCTGGGTCTACAT	22219

Sbjct	26718		TCCTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCCTCCTGGGTCTACAT	26777
Query	22220		CAGAGAGTACCTTTACATTAGACACATCAACCACTCCCTCCTTG	22263
Sbjct	26778		CAGAGAGTACCTTTACATTAGACACATCAACCACTCCCTCCTTG	26821

---

Score = 775 bits (403), Expect = 0.0  
 Identities = 536/560 (95%), Gaps = 18/560 (3%)  
 Strand=Plus/Minus

Query	24772	ACCTCCAGCATAATGACAGAATCAGCAGAAATGATGATCAAGACACAAACAGATCCTCCT	24831
Sbjct	2106	ACCTCCAGCATAATGACAGAATCAGCAGAAATGATGATCAAGACACAAACAGATCCTCCT	2047
Query	24832	GGGTCTACACCAGAGAGTACTCATACTGTGGACATATCAACAACACCCAACTGGGTAGAA	24891
Sbjct	2046	GGGTCTACACCAGAGAGTACTCATACTGTGGACATATCAACAACACCCAACTGGGTAGAA	1987
Query	24892	ACCCAC-TCGACT-GTGAC-TCAGAGATTTTCACACTCAGAGATGACCACTCTTGTGAGC	24948
Sbjct	1986	ACCCACTTCGACTNGTGACTTCAGAGATTTTGACACTCAGAGATGACCACTCTTGTGAGC	1927
Query	24949	-AGAAG-CCCTGG-TGAT-ATGTTAT--GGCCTAGTCAATCCTCTGTGGAAGAAACCAGC	25002
Sbjct	1926	TAGAAGCCCCTGGTTGATAATGTTATTGGGCTAGTCAATCCTCTGTGGAAGAAACCAGC	1867
Query	25003	TCTGCCTCTTCCCTGCTGTCTCTGCCTGCCACGACCTCACCTTC-TCCTGTTTCCTCTAC	25061
Sbjct	1866	TCTGCCTCTTCCCTGCTGTCTCTGCCTGCCACGACCTCACCTTCGTCCTGTTTCCTCTAC	1807
Query	25062	-ATTAGTAGAGG-ATTTCCCTTCCGCTTCTCTCCTGTGACTTCTCTTCTC-ACCCCT-G	25117
Sbjct	1806	AATTAGTAGAGGAATTTCCCTTCCGCTTCTCTCCTGTGACTTCTCTTCTCAACCCCTGG	1747
Query	25118	GCCTGGTGATAACCACAGACAGGATGGGCATAAGC-AGAGAA-CCTGGAACCAGTTCCAC	25175
Sbjct	1746	GCCTGGTGATAACCACAGACAGGATGGGCATAAGCAAGAGAAGCCTGGAACCAGTTCCAC	1687
Query	25176	TTCAAATTTGAGCAGCACCTCCCATGAGAGACTGACCACT-TTGGAAGACACTGTAGATA	25234
Sbjct	1686	TTCAAATTTGAGCAGCACCTCCCATGAGAGACTGACCACTGTTGGAAGACACTGTAGATA	1627
Query	25235	CAGAAGACATGCAGCCTTCCAC-ACACACAGCAGTGACCAACGTGAGGACCTCCATTCT	25293
Sbjct	1626	CAGAAGACATGCAGCCTTCCACAACACACAGCAGTGACCAACGTGAGGACCTCCATAACT	1567
Query	25294	GGACATGAATCACAATCTTC	25313
Sbjct	1566	GGAGCAGAATCACAATCTTC	1547

---

Score = 635 bits (330), Expect = 8e-177  
 Identities = 355/360 (98%), Gaps = 4/360 (1%)  
 Strand=Plus/Plus

Query	15574	AACACAGAAGAGACCAATGTGAAAGCCAACAACTCTGGACATGAATCCCATTCCCCTGCA	15633
Sbjct	29127	AACACAGAAGAGACCAATGTGAAAGCCAACAACTCTGGACATGAATCCCATTCCCCTGCA	29186
Query	15634	CTGGCTGACTCAGAGACACCCAAAGCCACAACCTCAAATGGTTATCACCACCACTGTGGGA	15693
Sbjct	29187	CTGGCTGACTCAGAGACACCCAAAGCCACAACCTCAAATGGTTATCACCACCACTGTGGGA	29246
Query	15694	GATCCAGCTCCTTCCACATCAATGCCAGTGCATGGTTCCTCTGAGACTACAAACATTAAG	15753
Sbjct	29247	GATCCAGCTCCTTCCACATCAATGCCAGTGCATGGTTCCTCTGAGACTACAAACATTAAG	29306
Query	15754	AGAGAGCCAACATATTCTTGACTCCTAG-CTGAGAGAGACCAGTACCTCTCAGGAGTC	15812
Sbjct	29307	AGAGAGCCAACATATTCTTGACTCCTAGAACTGAGAGAGACCAGTACCTCTCAGGAGTC	29366
Query	15813	CAGCTTTCCACGGACACAAGTTTTCTACTTTCCAAAGTCCCCACTGGTACTATTACTGA	15872
Sbjct	29367	CAGCTTTCCACGGACACAAGTTTTCTACTTTCCAAAGTCCCCACTGGTACTATTACTGA	29426
Query	15873	GGTCTCCAGTACAGGG-GTCAACTCTTCTAGCAAAATTTCCA--CCCCAGACCATGATAA	15929
Sbjct	29427	GGTCTCCAGTACAGGGNGTCATCTCTTCTAGCAAAATTTCCANNCCCCAGACCATGATAA	29486

---

Score = 619 bits (322), Expect = 3e-172  
 Identities = 335/339 (98%), Gaps = 2/339 (0%)  
 Strand=Plus/Plus

Query	16580	CCACCCTGGGGGACACAAGTGTTTCCACATCAACTCCTAATATCTCTCAGACTAACCAAA	16639
Sbjct	8229	CCACCCTGGGGGACACAAGTGTTTCCACATCAACTCCTAATATCTCTCAGACTAACCAAA	8288
Query	16640	TTCAAACAGAGCCAACAGCATCCCT--GAGCCCTAGACTGAGGGAGAGCAGCACGTCTGA	16697
Sbjct	8289	TTCAAACAGAGCCAACAGCATCCCGTGGAGCCCTAGACTGAGGGAGAGCAGCACGTCTGA	8348
Query	16698	GAAGACCAGCTCAACAACAGAGACAAATACTGCCTTTTCTTATGTGCCACAGGTGCTAT	16757
Sbjct	8349	GAAGACCAGCTCAACAACAGAGACAAATACTGCCTTTTCTTATGTGCCACAGGTGCTAT	8408
Query	16758	TACTCAGGCCTCCAGAACAGAAATCTCCTCTAGCAGAACATCCATCTCAGACCTTGATCG	16817
Sbjct	8409	TACTCAGGCCTCCAGAACAGAAATCTCCTCTAGCAGAACATCCATCTCAGACCTTGATCG	8468
Query	16818	GCCCACAATAGCACCCGACATCTCCACAGGAATGATCACCAGGCTCTTCACCTCCCCCAT	16877
Sbjct	8469	GTCCACAATAGCACCCGACATCTCCACAGGAATGATCACCAGGCTCTTCACCTCCCCCAT	8528
Query	16878	CATGACAAAATCTGCAGAAATGACCGTCACCACTCAAAC	16916
Sbjct	8529	CATGACAAAATCTGCAGAAATGACCGTCACCACTCAAAC	8567

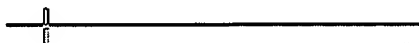
---

Score = 440 bits (229), Expect = 2e-118



Identities = 245/248 (98%), Gaps = 2/248 (0%)  
Strand=Plus/Plus

Query	9858	CCCAGAGATCAGGTCCACTGTGCGAAATTCTCCTTGGGAAGACTCCAGAAACAACTGTTCC	9917
Sbjct	29795	CCCAGAGATCAGGTC-ACTGTGAGAAATTCTCCTTGGGAAGACTCCAGAAACAACTGTTCC	29853
Query	9918	CATGGAGACCACAG-TGGAACCAGTCACCCTTCAGTCCACAGCCCTAGGAAGTGGCAGCA	9976
Sbjct	29854	CATGGAGACCACAGNTGGAACCAGTCACCCTTCAGTCCACAGCCCTAGGAAGTGGCAGCA	29913
Query	9977	CCAGCATCTCTCACCTGCCCACAGGAACCACATCACCAACCAAGTCACCAACAGAAAATA	10036
Sbjct	29914	CCAGCATCTCTCACCTGCCCACAGGAACCACATCACCAACCAAGTCACCAACAGAAAATA	29973
Query	10037	TGTTGGCTACAGAAAGGGTCTCCCTCTCCCCATCCCCACCTGAGGCTTGGACCAACCTTT	10096
Sbjct	29974	TGTTGGCTACAGAAAGGGTCTCCCTCTCCCCATCCCCACCTGAGGCTTGGACCAACCTTT	30033
Query	10097	ATTCTGGA 10104	
Sbjct	30034	ATTCTGGA 30041	



Score = 392 bits (204), Expect = 7e-104  
Identities = 245/253 (96%), Gaps = 8/253 (3%)  
Strand=Plus/Plus

Query	6320	ATTCCACAATCAGTAGGAGGAATGCAATCACTTCCTGGCTATGGGACCTCACTACATCTC	6379
Sbjct	33013	ATTCCACAATCAGTAGGAGGAATGCAATCACTTCCTGGCTATGGGACCTCACTACATCTC	33072
Query	6380	TCCCCACTACAACCTGGCCAAGTACTAGTTTATCTGAGGCACTGTCCTCAGGCCATTCTG	6439
Sbjct	33073	TCCCCACTACAACCTGGCCAAGTACTAGTTTATCTGAGGCACTGTCCTCAGGCCATTCTG	33132
Query	6440	GGGTTTCAAACCCAAGTTCAACTACGACTGAATTTCCACTCTTTTCAGCTGCATCCACAT	6499
Sbjct	33133	GGGTTTCAAACCCAAGTTCAACTACGACTGAATTTCCACTCTTTTCAGCTGCATCCACAT	33192
Query	6500	CTGCTGCTAAGCAA-AGAAATC-CAGAA--ACAGAGACCCATGGTCCC--CAGAATAC--	6551
Sbjct	33193	CTGCTGCTAAGCAACAGAAATCNCAGAANNACAGAGACCCATGGTCCCNNCAGAATACNN	33252
Query	6552	AGCCGCGAGTACT 6564	
Sbjct	33253	AGCCGCGAGTACT 33265	



Score = 369 bits (192), Expect = 6e-97  
Identities = 493/636 (77%), Gaps = 5/636 (0%)  
Strand=Plus/Plus

Query	24247	ACAGATATGTTGCACAAAAGCTCAGAACCTGTAACCAACTCACCTGCAAATTTGAGCAGC	24306
Sbjct	26182	ACAGACATGTTACACAAAGCCCAGAAC-TGTAACCAG-TCACCTCCAAAGCTGAGCCAC	26239



Query	25424	GAATTCAGATAGAACCAACATCCTCCCTGACTTCTGGATTGAGGGAGACCAGCAGCTCTG	25483
Sbjct	26472	GAATTCAGAAAGAGTCAATTTCTCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTG	26531
Query	25484	AGAGGATCAGCTCAGCCACAGAGGGAAGCACTGTCCTTTCTGAAGTGCCAGTGGTGCTA	25543
Sbjct	26532	TGGAGACAAGCTCAGCCATAGAGACAAGTGCTGTCCTTTCTGAAGTGTCGGTTGGTGCTA	26591
Query	25544	CCACTGAGGTCTCCAGGACAGAAGTGATATCCTCTAGGGGAACATCCATGTCAGGGCCTG	25603
Sbjct	26592	CTACTGAGATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTG	26651
Query	25604	ATCAGTTTACCATATCACCAGACATCTCTA-CTGAAG--CGATCACCAGGCTTTCTACTT	25660
Sbjct	26652	CTGAGTCCACAATGTTGCCAGAAATATCCACCACAAGAAAAATCATTAAGTTCCTACTT	26711
Query	25661	CCCCATTATGACAGAATCAGCAGAAAGTGCCATCACTATTGAGACAGGTTCTCCTGGGG	25720
Sbjct	26712	CCCCATCCTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCCTCCTGGGT	26771
Query	25721	CTACATCAGAGGTACCCTCACCTTGGACACCTCAAC	25757
Sbjct	26772	CTACATCAGAGGTACCTTTACATTAGACACATCAAC	26808

---

Score = 296 bits (154), Expect = 6e-75  
Identities = 479/634 (75%), Gaps = 5/634 (0%)  
Strand=Plus/Plus

Query	20735	CCACAGACACATTGGGCACAAGCCCAGAACCTACAACCAGTTCACCTCCAAATTTGAGCA	20794
Sbjct	26180	CCACAGACATGTTACACACAAGCCCAGAAC-TGTAACCAGT-CACCTCCAAAGCTGAGCC	26237
Query	20795	GTACCTCACATGTGATACTGACAACAGATGAAGACACCACAGCTATAGAAGCCATGCATC	20854
Sbjct	26238	ACACTTCACATGAGAGACTGACCACTGGCAAGGACACCACAAATACAGAAGCTGTGCATC	26297
Query	20855	CTTCCACAAGCACAGCAGCGACTAATGTGGAACACACCTGTTCTGGACATGGGTCACAAT	20914
Sbjct	26298	CTTCCACAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTCTGGACATGAATCCCCTT	26357
Query	20915	CCTCTGTCTAACTGACTCAGAAAAACCAAGGCCACAGCTCCAATGGATACCACCTCCA	20974
Sbjct	26358	CCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATACCAATGTTTATTACCTCCA	26417
Query	20975	CCATGGGGCATACTAAGTGTTCACATCAATGTCTGTTTCTGAGACTACAAAAATTA	21034
Sbjct	26418	CCCAGGAGGATACAACTGTTGCCATATCAACCCCTCACTTCTTGGAGACTAGCAGAATTC	26477
Query	21035	AGAGAGAGTCAACATATTCCTTGACTCCTGGACTGAGAGAGACCAGCATTTCCCAAATG	21094
Sbjct	26478	AGAAAGAGTCAATTTCTCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTGGAGA	26537
Query	21095	CCAGCTTTTCCACTGACACAAGTATTGTTCTTTTCTGAGAAGTCCCCACTGGTACTACTGCTG	21154
Sbjct	26538	CAAGCTCAGCCATAGAGACAAGTGCTGTCCTTTCTGAAGTGTCGGTTGGTGTACTACTG	26597
Query	21155	AGGTCTCCAGGACAGAAGTCACCTCCTCTGGTAGAACATCCATCCCTGGCCCTTCTCAGT	21214
Sbjct	26598	AGATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTGCTGAGT	26657

Query	21215	CCACAGTTTTGCCAGAAATAT---CCACAAGAACAATGACAAGGCTCTTTGCCTCGCCCA	21271
Sbjct	26658	CCACAATGTTGCCAGAAATATCCACCACAAGAAAAATCATTAAGTTCCTACTTCCCCCA	26717
Query	21272	CCATGACAGAATCAGCAGAAATGACCATCCCCACTCAAACAGGTCCTTCTGGGTCTACCT	21331
Sbjct	26718	TCCTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCCTCCTGGGTCTACAT	26777
Query	21332	CACAGGATACCCTTACCTTGGACACATCCACCAC	21365
Sbjct	26778	CAGAGAGTACCTTTACATTAGACACATCAACCAC	26811

---

Score = 291 bits (151), Expect = 3e-73  
Identities = 155/157 (98%), Gaps = 0/157 (0%)  
Strand=Plus/Minus

Query	17160	AGAGAGCATCCCCTCCTCTCCTCTCCCTGTGACTGCACTTCTTACTTCTGTTCTGGTGAC	17219
Sbjct	8725	AGAGAGCATCCCCTCCTCTCCTCTCCCTGTGACTGCACTTCTTACTTCTGTTCTGGTGAC	8666
Query	17220	AACCACCAATGTATTGGGCACAACAAGCCCAGAGACCGTAACGAGTTCACCTCCAAATTT	17279
Sbjct	8665	AACCACAAATGTATTGGGCACAACAAGCCCAGAGCCCGTAACGAGTTCACCTCCAAATTT	8606
Query	17280	AAGCAGCCCCACACAGGAGAGACTGACCACTTACAAA	17316
Sbjct	8605	AAGCAGCCCCACACAGGAGAGACTGACCACTTACAAA	8569

---

Score = 266 bits (138), Expect = 1e-65  
Identities = 397/524 (75%), Gaps = 3/524 (0%)  
Strand=Plus/Plus

Query	22624	CATCCTTTCCCAAACACGGCAGTAACCAAAGTTGGAACCTCCAGTTCTGGACATGAATCC	22683
Sbjct	26294	CATCCTTCCAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTCTGGACATGAATCC	26353
Query	22684	CCTTCCTCTGTCTACCTGACTCAGAGACAACCAAAGCCACATCGGCAATGGGTACCATC	22743
Sbjct	26354	CCTTCCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTACC	26413
Query	22744	TCCATTATGGGGGATACAAGTGTCTTCTACATTAACCTCCTGCCTTATCTAACACTAGGAAA	22803
Sbjct	26414	TCCACCCAGGAGGATACAACCTGTTGCCATATCAACCCCTCACTTCTTGGAGACTAGCAGA	26473
Query	22804	ATTCAGTCAGAGCCAGCTTCTCACTGACCACCAGATTGAGGGAGACCAGCACCTCTGAA	22863
Sbjct	26474	ATTCAGAAAGAGTCAATTTCTCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTG	26533
Query	22864	GAGACCAGCTTAGCCACAGAAGCAAACACTGTTCTTTCTAAAGTGTCCACTGGTGCTACT	22923
Sbjct	26534	GAGACAAGCTCAGCCATAGAGACAAGTGCTGCTTTCTGAAGTGTCCGTTGGTGCTACT	26593
Query	22924	ACTGAGGTCTCCAGGACAGAAGCCATCTCCTTTAGCAGAACATCCATGTCAGGCCCTGAG	22983